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OM protein - protein search, using sw model

Run on : May 7, 2002, 11:58:52 ; Search time 26.38 Seconds

(without alignments)
190.229 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGQFRHKAQQLNLATRWW.....MPTEPECEBKQFQPYFIPIN 223

Scoring table: BL050462

Gapext: 0.5

Searched: 212252 seqs, 22503292 residues

All number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/podata/2/iaa/5A_COMB_pep:*

2: /cgn2_6/podata/2/iaa/5B_COMB_pep:*

3: /cgn2_6/podata/2/iaa/6A_COMB_pep:*

4: /cgn2_6/podata/2/iaa/6B_COMB_pep:*

5: /cgn2_6/podata/2/iaa/PCNUS_COMB_pep:*

6: /cgn2_6/podata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1158	98.6	223	3	US-09-228-208A-17	Sequence 17, Appl
2	1103.5	94.0	234	1	US-08-505-1	Sequence 1, Appl
3	1103.5	94.0	234	2	US-08-459-818-21	Sequence 21, Appl
4	1103.5	94.0	234	2	US-08-889-666-21	Sequence 21, Appl
5	1103.5	94.0	234	2	US-08-465-078-21	Sequence 21, Appl
6	1103.5	94.0	234	2	US-08-725-776-21	Sequence 21, Appl
7	1103.5	94.0	234	2	US-08-488-062-21	Sequence 21, Appl
8	970	82.6	187	1	US-08-057-684-14	Sequence 14, Appl
9	970	82.6	187	1	US-08-008-898-14	Sequence 14, Appl
10	970	82.6	187	2	US-08-459-818-14	Sequence 14, Appl
11	970	82.6	187	2	US-08-889-666-14	Sequence 14, Appl
12	970	82.6	187	2	US-08-465-078-14	Sequence 14, Appl
13	970	82.6	187	2	US-08-725-776-14	Sequence 14, Appl
14	970	82.6	187	2	US-08-488-062-14	Sequence 22, Appl
15	967	82.4	187	3	US-08-228-208A-14	Sequence 14, Appl
16	967	82.4	187	5	PCT-US95-06726-36	Sequence 36, Appl
17	857	73.0	223	3	US-08-228-208A-18	Sequence 18, Appl
18	804.5	68.5	234	1	US-08-505-058-2	Sequence 2, Appl
19	804.5	68.5	187	2	US-08-459-818-22	Sequence 22, Appl
20	804.5	68.5	234	2	US-08-488-062-14	Sequence 22, Appl
21	804.5	68.5	234	2	US-08-465-078-22	Sequence 22, Appl
22	804.5	68.5	234	2	US-08-725-776-22	Sequence 22, Appl
23	804.5	68.5	234	2	US-08-488-062-22	Sequence 22, Appl
24	648	55.2	124	4	US-08-530-172-4	Sequence 4, Appl
25	648	55.2	357	3	US-08-630-172-20	Sequence 4, Appl
26	648	55.2	357	4	US-09-375-419-20	Sequence 20, Appl
27	648	55.2	357	4	US-08-228-208A-17	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-228-208A-17
; Sequence 17, Application US/08228208A

; GENERAL INFORMATION:

; ; PATENT NO. 6090944
; ; APPLICANT: Linsley, Peter S.
; ; APPLICANT: Ledbetter, Jeffrey A.
; ; APPLICANT: Damle, Nitin K.
; ; APPLICANT: Brady, William
; ; APPLICANT: Wallace, Phillip M.
; ; TITLE OF INVENTION: CTLA4/CD28/B19 HYBRID FUSION
; ; NUMBER OF SEQUENCES: 22
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Merchant & Gould
; ; STREET: 11150 Santa Monica Boulevard, Suite 400
; ; CITY: Los Angeles
; ; STATE: CA
; ; COUNTRY: USA
; ; ZIP: 90025

; COMPUTER READABLE FORM:

; ; MEDIUM TYPE: Diskette
; ; COMPUTER: IBM Compatible
; ; OPERATING SYSTEM: DOS
; ; SOFTWARE: FASTSEQ Version 2.0
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/08/228,208A
; ; FILING DATE: 15-APR-1994
; ; CLASSIFICATION: 435
; ; PRIOR APPLICATION DATA:
; ; APPLICATION NUMBER: 08/008,898
; ; FILING DATE: 22-JAN-1993
; ; APPLICATION NUMBER: 07/723,617
; ; FILING DATE: 27-JUN-1991
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Adriano, Sarah B.
; ; REGISTRATION NUMBER: 34,470
; ; REFERENCE/DOCKET NUMBER: 30436-30US01
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 310 445-1140
; ; TELEFAX: 310 445-9031
; ; INFORMATION FOR SEQ ID NO: 17:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 223 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: unknown
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; US-08-228-208A-17

Query Match 98.6%; Score 1158; DB 3; Length 223;
 Best Local Similarity 98.7%; Pred. No. 3. 4e-111; Indels 0; Gaps 0;
 Matches 220; Conservative 0; Mismatches 3; Delins 0;

1 MACLGFORHKQAOLNLAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 60
 1 MACLGFORHKQAOLNLAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 60

Qy 1 MACLGFORHKQAOLNLAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 60
 Db 1 MACLGFORHKQAOLNLAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 60

61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGLR 1.20
 1 MACLGFORHKQAOLNLAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 60

Qy 61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGLR 1.20
 Db 61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGLR 1.20

61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGLR 1.20
 1 MACLGFORHKQAOLNLAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 60

Qy 61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGLR 1.20
 Db 61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGLR 1.20

121 AMDTGLYICKVELMPPYYLGIGNGAQIYVDPPECPDSDDEFLWILAVSSCLFFYSL 180
 121 AMDTGLYICKVELMPPYYLGIGNGAQIYVDPPECPDSDDEFLWILAVSSCLFFYSL 180

Db 121 AMDTGLYICKVELMPPYYLGIGNGAQIYVDPPECPDSDDEFLWILAVSSCLFFYSL 180

RESULT 3
 US-08-459-818-21
 Sequence 21. Application US/08459818
 ; Patient No. 5851795
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.
 ; ADDRESSER: Merchant & Gould
 ; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/505,058
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/228,208
 ; FILING DATE: 15-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adriano, Sarah B.
 ; REGISTRATION NUMBER: 34,470
 ; REFERENCE/DOCKET NUMBER: 30436-35US02
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-445-9031
 ; TELEX/FAX: 310-445-9031
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 234 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-459-818-21

Query Match 94.0%; Score 1103.5; DB 1; Length 234;
 Best Local Similarity 94.0%; Pred. No. 1.4e-105; Indels 11; Gaps 5;
 Matches 220; Conservative 0; Mismatches 3;

1 MACLGFORHKQAOLNIAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 6
 1 MACLGFORHKQAOLNIAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 6

61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGL 1
 1 MACLGFORHKQAOLNIAATRWPCTLLFPLFLFVPECKAMHVAQPAVVLASSRGIAASFYCEY 6

Qy 61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGL 1
 Db 61 ASPGKATEVRVTVLROADSQTVECAATYMMGNELTFLDDSTCCTGTSSGNOVNLTIOGL 1

QY 119 LRAMDTGLYICKVELMPPPYL-GIGNGAQIYVDPPEC-----PDSDFLLWILAAVSS 172
 Db 121 LRAMDTGLYICKVELMPPPYL-GIGNGAQIYVDPPECXXXXXPDSDFLLWILAAVSS 180

QY 173 GLFFYSFLLT-AVSLSKMLKRSPLTTCGVYKMPTEPECE--KQFQYFIPIN 223
 Db 181 GLFFYSFLLTAVSLSKMLKRSPLTTCGVYKMPTEPECEXXKQFQYFIPIN 234

RESULT 5
 US-08-465-078-21.
 Sequence 21. Application US/08465078
 Patent No. 5885796

GENERAL INFORMATION:
 APPLICANT: Linsley, Peter S.
 APPLICANT: Ledbetter, Jeffrey A.
 APPLICANT: Damle, Nitin K.
 APPLICANT: Brady, William
 APPLICANT: Kienker, Peter A.

TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 11150 Santa Monica Blvd., Suite 400
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/465,078
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/375390
 FILING DATE: 18-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 234 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-465-078-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
 Best Local Similarity 94.0%; Pred. No. 1.4e-105; Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAGUNLAIRTPWTLFLFLFLFIPVECKAMHVQPAVVLASSRGASFVCEY 60
 Db 1 MACLGFORHKAGUNLAIRTPWTLFLFLFLFIPVECKAMHVQPAVVLASSRGASFVCEY 60

QY 61 ASPGKATEVRVTVLROADSQTVECAATYGMGNELFLDDS--ICTGTSSGQVNLTQG 118
 Db 61 ASPGKATEVRVTVLROADSQTVECAATYGMGNELFLDDSXXCTGTSSGQVNLTQG 120

QY 119 LRAMDTGLYICKVELMPPPYL-GIGNGAQIYVDPPEC-----PDSDFLLWILAAVSS 172
 Db 121 LRAMDTGLYICKVELMPPPYLXGIGNTQIVYDPECEXXKQFQYFIPIN 223

QY 173 GLFFYSFLLT-AVSLSKMLKRSPLTTCGVYKMPTEPECE--KQFQYFIPIN 223
 Db 181 GLFFYSFLLTAVSLSKMLKRSPLTTCGVYKMPTEPECEXXKQFQYFIPIN 234

RESULT 6
 US-08-725-776-21
 ; Sequence 21, Application US/08725776
 ; Patent No. 5988510
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Damle, Nitin K.
 ; APPLICANT: Brady, William K.
 ; APPLICANT: Kiener, Peter A.
 ; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/725,776
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION NUMBER: US 08/375390
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adriano, Sarah B.
 ; REGISTRATION NUMBER: 34,470
 ; REFERENCE/DOCKET NUMBER: 30436-35US01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-445-1140
 ; TELEFAX: 310-445-9031
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 234 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-488-062-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
 Best Local Similarity 94.0%; Pred. No. 1.4e-105; Gaps 5;
 Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKQNLNATRWTCTTFLFLPVECKAMHVQPAVVLASSRGIAASPVCEY 60
 Db 1 MACLGFORHKQNLNATRWTCTTFLFLPVECKAMHVQPAVVLASSRGIAASPVCEY 60
 QY 61 ASPGKATEVRVTLROADSQTTEVCAATYMMGNELTFLDDS - ICNGTSSGNQNLTIG 118
 Db 61 ASPGKATEVRVTLROADSQTTEVCAATYMMGNELTFLDDXXCTGTSSGNQNLTIG 120
 QY 119 LRMDTGLYICKVELMPPPYL-GIGNGAQTYYVIDPEPC----PDSDFLWLIAVSS 172
 Db 121 LRMDTGLYICKVELMPPPYLXGIGNTQIYVIDPEPCXXKOFQYFIPIN 223
 QY 173 GLFFYSFLLT-AVLSKMLKRSPLTTGYYKMPTEPECE--KOFQYFIPIN 223
 Db 181 GLFFYSFLLTAVLSKMLKRSPLTTGYYKMPTEPECEXXKOFQYFIPIN 234

RESULT 8
 US-08-067-684-14
 ; Sequence 14, Application US/08067684
 ; Patent No. 534131
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.

APPLICANT: Ledbetter, Jeffrey A.
 ;
 ; APPLICANT: Damle, Nitin K.
 ; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheldon & Mak
 ; STREET: 225 South Lake Avenue, Suite 900
 ; CITY: Pasadena
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 91101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/067,684
 ; FILING DATE: 26-MAY-1993
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adriano, Sarah B.
 ; REGISTRATION NUMBER: 34,470
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310/312-9900
 ; FAX: 310/479-8340
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 187 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: No
 ; ANTI-SENSE: No
 ; US-08-067-684-14

Query Match 82.6%; Score 970; DB 1; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92;
 Matches 186; Conservative 0; Mismatches 0; Gaps 0;

QY 37 AMHQAPAVVLAASSRGIASTVCEASPGKATEEVRYTVLROADSQTVECAATYMMGNELT 96
 Db 1 AMHQAPAVVLAASSRGIASTVCEASPGKATEEVRYTVLROADSQTVECAATYMMGNELT 60

QY 97 FLDDSICGTSGNQVNLTIGLARDTGLYICKVELMPPYYLGIGNGAQIYVDPEP 156
 Db 61 FLDDSICGTSGNQVNLTIGLARDTGLYICKVELMPPYYLGIGNGQIYVDPEP 120

QY 157 CPDSDFLLWILAAVSSGLFFYSFLLTAVSLSKMLKKSPLTTGYYVKMPTEPECEKQFQ 216
 Db 121 CPDSDFLLWILAAVSSGLFFYSFLLTAVSLSKMLKKSPLTTGYYVKMPTEPECEKQFQ 180

QY 217 PYFIPIN 223
 Db 181 PYFIPIN 187

RESULT 10
 US-08-459-818-14
 ; Sequence 14, Application US/08459818

RESULT 9
 US-08-008-8198-14
 ; Sequence 14, Application US/08008898

; General Information:
 ; APPLICANT: Linsley, Peter S.
 ; PATENT NO. 5,770,917

; General Information:
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Damle, Nitin K.

; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheldon & Mak

Query Match 82.6%; Score 970; DB 1; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92;
 Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 37 AMHQAPAVVLAASSRGIASTVCEASPGKATEEVRYTVLROADSQTVECAATYMMGNELT 96
 Db 1 AMHQAPAVVLAASSRGIASTVCEASPGKATEEVRYTVLROADSQTVECAATYMMGNELT 60
 QY 97 FLDDSICGTSGNQVNLTIGLARDTGLYICKVELMPPYYLGIGNGAQIYVDPEP 156
 Db 61 FLDDSICGTSGNQVNLTIGLARDTGLYICKVELMPPYYLGIGNGQIYVDPEP 120
 QY 157 CPDSDFLLWILAAVSSGLFFYSFLLTAVSLSKMLKKSPLTTGYYVKMPTEPECEKQFQ 216
 Db 121 CPDSDFLLWILAAVSSGLFFYSFLLTAVSLSKMLKKSPLTTGYYVKMPTEPECEKQFQ 180
 QY 217 PYFIPIN 223
 Db 181 PYFIPIN 187

RESULT 10
 US-08-459-818-14
 ; Sequence 14, Application US/08459818

GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Damle, Nitin K.

TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 1150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90025
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FastSeq 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459, 818
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-459-818-14

Query Match 82.6%; Score 970; DB 22; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92; Indels 0; Gaps 0;
 Matches 186; Conservative 0; Mismatches 1; Del 0; Insert 0;

Query Match 82.6%; Score 970; DB 22; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92; Indels 0; Gaps 0;
 Matches 186; Conservative 0; Mismatches 1; Del 0; Insert 0;

QY 37 AMHVAQPAVLLASSRGIAFSEYASPQKATEVRVTLROADSQTEVCATYMMGNELT 96
 Db 1 AMHVAQPAVLLASSRGIAFSEYASPQKATEVRVTLROADSQTEVCATYMMGNELT 60

QY 97 FLDSICITGTSQQNVTIQTGRMTGLYCKVELMPPYYLGINQAGIYVIDPEP 156
 Db 61 FLDSICITGTSQQNVTIQTGRMTGLYCKVELMPPYYLGINQAGIYVIDPEP 120

QY 157 CPDSDFLWILWLAAYSSGLEFFYSFLLTAVSLSKMLKRSPLTGVYKMPTEPECEKQFQ 216
 Db 121 CPDSDFLWILWLAAYSSGLEFFYSFLLTAVSLSKMLKRSPLTGVYKMPTEPECEKQFQ 180

QY 217 PYFIPIN 223
 Db 181 PYFIPIN 187

RESULT 12
 US-08-459-818-14
 Sequence 14, Application US/08465078
 Patent No. 5885796

GENERAL INFORMATION:
 APPLICANT: Linsley, Peter S.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Ledbetter, Jeffrey A.
 APPLICANT: Dame, Nitin K.
 APPLICANT: Brady, William
 APPLICANT: Kienner, Peter A.

TITLE OF INVENTION: CTIA4 Receptor and Uses Thereof
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 11150 Santa Monica Blvd., Suite 400
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465, 078
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/375390
 FILING DATE: 18-JAN-1995
 ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/375390
 FILING DATE: 18-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-889-666-14

Query Match 82.6%; Score 970; DB 22; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92; Indels 0; Gaps 0;
 Matches 186; Conservative 0; Mismatches 1; Del 0; Insert 0;

QY 37 AMHVAQPAVLLASSRGIAFSEYASPQKATEVRVTLROADSQTEVCATYMMGNELT 96
 Db 1 AMHVAQPAVLLASSRGIAFSEYASPQKATEVRVTLROADSQTEVCATYMMGNELT 60

QY 97 FLDSICITGTSQQNVTIQTGRMTGLYCKVELMPPYYLGINQAGIYVIDPEP 156
 Db 61 FLDSICITGTSQQNVTIQTGRMTGLYCKVELMPPYYLGINQAGIYVIDPEP 120

QY 157 CPDSDFLWILWLAAYSSGLEFFYSFLLTAVSLSKMLKRSPLTGVYKMPTEPECEKQFQ 216
 Db 121 CPDSDFLWILWLAAYSSGLEFFYSFLLTAVSLSKMLKRSPLTGVYKMPTEPECEKQFQ 180

QY 217 PYFIPIN 223
 Db 181 PYFIPIN 187

RESULT 12
 Sequence 14, Application US/08465078
 Patent No. 5885796

GENERAL INFORMATION:
 APPLICANT: Linsley, Peter S.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Ledbetter, Jeffrey A.
 APPLICANT: Dame, Nitin K.
 APPLICANT: Brady, William
 APPLICANT: Kienner, Peter A.

TITLE OF INVENTION: CTIA4 Receptor and Uses Thereof
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 11150 Santa Monica Blvd., Suite 400
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465, 078
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/375390
 FILING DATE: 18-JAN-1995
 ATTORNEY/AGENT INFORMATION:

NAME: Adriano, Sarah B. ; TELEFAX: 310-445-9031 ; INFORMATION FOR SEQ ID NO: 14;

REGISTRATION NUMBER: 34,470 ; SEQUENCE CHARACTERISTICS:

TELECOMMUNICATION INFORMATION: ; LENGTH: 187 amino acids

TELEPHONE: 310-445-1140 ; TYPE: amino acid

INFORMATION FOR SEQ ID NO: 14 : ; TOPOLOGY: linear

SEQUENCE CHARACTERISTICS: ; MOLECULE TYPE: protein

LENGTH: 187 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-465-078-14

Query Match Score 970; DB 2; Length 187; Best Local Similarity 99.5%; Pred. No. 5.1e-92; Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AMHVAQPAVVLASSRGTSASFYCEASPGKATEVRVTVLROADSQTVTFCATYMMGNELT 96
1 AMHVAQPAVVLASSRGTSASFYCEASPGKATEVRVTVLROADSQTVTFCATYMMGNELT 60

FLDDSICGTGSSGNVNLTIGLRRMTGLYICKVEMYPPPYLGNGAQIYVIDPEP 156
97 FLDDSICGTGSSGNVNLTIGLRRMTGLYICKVEMYPPPYLGNGAQIYVIDPEP 120

CPDSDFELWILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYKMPPECEKQFQ 216
61 CPDSDFELWILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYKMPPECEKQFQ 180

CPDSDFELWILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYKMPPECEKQFQ 216
157 CPDSDFELWILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYKMPPECEKQFQ 120

PYFIPIN 223
121 CPDSDFELWILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYKMPPECEKQFQ 180

PYFIPIN 223
181 PYFIPIN 187

RESULT 14 US-08-488-062-14

Sequence 14, Application US/08488062
Patent No. 5977318

GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William A.
APPLICANT: Kiener, Peter A.

TITLE OF INVENTION: CTIA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION:
CLASSIFICATION: 435
APPLICATION NUMBER: US/08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid

NAME: Adriano, Sarah B. ; REGISTRATION NUMBER: 34,470 ; REFERENCE/DOCKET NUMBER: 30436-35US01

TELECOMMUNICATION INFORMATION: ; TELEPHONE: 310-445-1140

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-062-14

Query Match 82.6%; Score 970; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92;
 Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 37 AMHVAOPAVLASSRGTAASFCEYASPGKATEVRVTLROADSQTVECAATYMGNELT 96
 DB 1 AMHVAOPAVLASSRGTAASFCEYASPGKATEVRVTLROADSQTVECAATYMGNELT 60
 QY 97 FLDDSDICGTGSSGNQVNLTIGGLRADMGTGLYICKVELMPPYYLIGNGAQIYVIDPEP 156
 DB 61 CPDSDFLIWILAVSSGLFFYSFLTAVSLSKMLKRSPLTTGGYVKKMPPTEPECEKQFQ 216
 QY 157 CPDSDFLIWILAVSSGLFFYSFLTAVSLSKMLKRSPLTTGGYVKKMPPTEPECEKQFQ 216
 DB 121 CPDSDFLIWILAVSSGLFFYSFLTAVSLSKMLKRSPLTTGGYVKKMPPTEPECEKQFQ 180
 D 217 PYFIPIN 223
 D 181 PYFIPIN 187

RESULT 15
 US-08-228-208A-14
 Sequence 14, Application US/08228208A

; GENERAL INFORMATION:

; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Damle, Nitin K.
 ; APPLICANT: Brady, William M.
 ; APPLICANT: Wallace, Phillip M.
 TITLE OF INVENTION: CMLA4/CD28 Ig HYBRID FUSION
 TITLE OF INVENTION: PROTEINS AND USES THEREOF
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESS: Merchant & Gould
 STREET: 11150 Santa Monica Boulevard, Suite 400
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA

; ZIP: 90025
 COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/228,208A

; FILING DATE: 15-APR-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/008,898

; FILING DATE: 22-JAN-1993

; APPLICATION NUMBER: 07/723,617

; FILING DATE: 27-JUN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Adriano, Sarah B.
 ; REGISTRATION NUMBER: 34,470
 ; REFERENCE/DOCKET NUMBER: 30436-30US01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 310 445-1140

; TELEFAX: 310 445-9031

; TELEX:
 ; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 187 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein
 ; US-08-228-208A-14

Query Match 82.6%; Score 970; DB 3; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92;
 Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 1 AMHVAOPAVLASSRGIAFSVGEYASPGKATEVRVTLROADSQTVECAATYMGNELT 60
 QY 97 FLDDSDICGTGSSGNQVNLTIGGLRADMGTGLYICKVELMPPYYLIGNGAQIYVIDPEP 156
 DB 61 FLDDSDICGTGSSGNQVNLTIGGLRADMGTGLYICKVELMPPYYLIGNGAQIYVIDPEP 120
 QY 157 CPDSDFLIWILAVSSGLFFYSFLTAVSLSKMLKRSPLTTGGYVKKMPPTEPECEKQFQ 216
 DB 121 CPDSDFLIWILAVSSGLFFYSFLTAVSLSKMLKRSPLTTGGYVKKMPPTEPECEKQFQ 180
 D 217 PYFIPIN 223
 D 181 PYFIPIN 187

Search completed: May 7, 2002, 12:01:21
 Job time: 149 sec

A; Reference number: 146689; MUID:95369849
 A; Accession: I46696
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 1-223 <ISO>
 A; Cross-references: GB:D49844; NID:9755100; PID:BAA08644.1; MUID:9755101
 C; Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

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 Best Local Similarity 84.3%; Pred. No. 4.7e-85;
 Matches 188; Conservative 16; Indels 0; Gaps 0;

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 Db 1 MARIGFQRGQTOLDLQSITWSGAALFSTLFLFVSKAHVSPAVVLAASSRGVASFVCEY 60

QY 61 ASPGKATEVRVTYLROADSQTVECAATYMMGNELFLDDSTCTGTSSGGNOVNLTQGLR 120
 R; Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, P.; Golstein, P.
 C; Date: 21-May-1998 #sequence_revision 21-May-1998 #text_change 05-Nov-1999
 C; Species: Mus musculus (house mouse)
 C; Accession: A29063; I49622
 R; Brunet, J.F.; Denizot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.
 Nature 328, 267-270, 1987
 A; Title: A new member of the immunoglobulin superfamily--CTLA-4.
 A; Reference number: A29063; MUID:87250259
 A; Accession: A29063
 A; Molecule type: mRNA
 A; Residues: 1-223 <ISO>
 A; Cross-references: GB:X05719; NID:950592; PID:CAA29191.1; PID:950593
 R; Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, P.; Golstein, P.
 J. Immunol. 147, 1037-1044, 1991
 A; Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
 A; Reference number: I49584; MUID:9131845
 A; Accession: I49622
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-36 <RE>
 A; Cross-references: GB:M74362; NID:9192833; PID:AAA37489.1; PID:9553903
 A; Gene: Ctla-4
 A; Map Position: 1; band C
 C; Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C; Keywords: transmembrane protein

RESULT 3
 S08614
 cytotoxic T-lymphocyte protein 4 - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
 C; Accession: S08614
 R; Darlavach, P.; Mattei, M.G.; Golstein, P.; Lefranc, M.P.
 Eur. J. Immunol. 18, 1901-1905, 1988
 A; Title: Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of prot
 A; Reference number: S08614; MUID:89120925
 A; Map Position: X15070; NID:9825649
 A; Molecule type: DNA
 A; Residues: 1-166 <DR>
 A; Cross-references: EMBL:X15070; PID:9825649
 C; Genetics:
 A; Gene: GDB:CTLA4
 A; Cross-references: GDB:119818; OMIM:123890
 A; Map Position: 2q33-2q33
 A; Introns: 116/1; 152/3
 C; Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C; Keywords: transmembrane protein
 F; 151-186/Domain: transmembrane #status Predicted <TM>
 F; 151-186/Domain: intracellular #status Predicted <INT>
 F; 21-92/Disulfide bonds: #status predicted

RESULT 3
 S25168
 CHT28 protein - chicken
 C; Species: Gallus gallus (chicken)
 C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C; Accession: S25168
 R; Young, J.R.; Davison, T.F.; Tregaskes, C.A.; Fennie, M.C.; Vainio, O.
 J. Immunol. 152, 3848-3851, 1994
 A; Title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.
 A; Reference number: 150619; MUID:9419147
 A; Accession: 150619
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 1-221 <O2>
 A; Cross-references: EMBL:X67915; NID:963221
 C; Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C; Keywords: transmembrane protein

Query Match 82.6%; Score 970; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1.2e-82; Indels 0; Gaps 0;

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 Db 1 MHYAQPAVVLASSRGIASFVCEYASPKATEVRVTYLROADSQTEVCAATYMMGNELTF 97

QY 98 LDDSICGTSQVNLTIAAYSGLFFYSFLTAVSLKRSPLTGVYKMPPTPECEKQFQYFIPIN 217
 Db 61 LDDSICGTSQVNLTIAAYSGLFFYSFLTAVSLKRSPLTGVYKMPPTPECEKQFQYFIPIN 217

QY 158 PDSDFLWILIAAYSGLFFYSFLTAVSLKRSPLTGVYKMPPTPECEKQFQYFIPIN 217
 Db 121 PDSDFLWILIAAVSSGLFFYSFLTAVSLKRSPLTGVYKMPPTPECEKQFQYFIPIN 180

QY 218 YFIPIN 223

GenCore version 4.5
 Copyright (c) 1993 - 2000 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: May 7, 2002, 12:01:22 ; Search time 19.81 Seconds
 (without alignments)
 412.734 Million cell updates/
 Title: US-09-772-103-2
 perfect score: 1174
 Sequence: 1 MACIGFRKIQALNQJATRW.....MPPTPECEKFOPYFIDTN 223

Scoring table: BLASTM62
Gapop 10.0 , Gapext 0.5
Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 1000050

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score obtained, and is derived by analysis of the total score distribution.

CERAMICS

Result No.	Score	Query	Match Length	DB ID	Description	
					CPL14_HUMAN	CPL14_PIG
1	1174	100.0	223	1	P16410	homo sapi
2	1010	86.0	223	1	Q9m7X	sus scrof
3	997	84.9	223	1	P42072	oryctolag
4	878	74.8	223	1	P09753	mus muscu
5	211	18.0	221	1	P10143	gallus ga
6	204	17.4	221	1	P42069	oryctolag
7	203	17.3	219	1	Q28071	bos tauru
8	187	15.9	220	1	P10747	homo sapi
9	170	14.5	218	1	P31041	rattus nor
10	156	13.3	218	1	CD28_MOUSE	homo sapi
11	91	7.8	4393	1	CD28_RAT	rattus nor
12	89.5	6.6	3707	1	P0BM_HUMAN	homo sapi
13	87	7.4	739	1	P0BM_MOUSE	mus muscu
14	86	7.3	739	1	V0A1_RAT	rattus nor
15	85	7.2	1356	1	V0A1_MOUSE	mus muscu
16	85	7.2	1367	1	VGR2_HUMAN	homo sapi
17	83	7.1	1111	1	LV2A_HUMAN	homo sapi
18	83	7.1	111	1	LV2D_HUMAN	homo sapi
19	83	7.1	1343	1	VGR2_RAT	rattus nor
20	82	7.0	215	1	CB2B_HUMAN	homo sapi
21	81.5	6.9	111	1	KV12_RABBIT	oryctolag
22	81.5	6.9	1897	1	PTPF_HUMAN	homo sapi
23	81	6.9	246	1	M0G_MOUSE	mus muscu
24	79.5	6.8	108	1	KV6K_MOUSE	equine her
25	79	6.7	550	1	VGL6_HSVEB	equine her
26	79	6.7	552	1	VGL6_HSVEL	equine her
27	78.5	6.7	108	1	KV1H_HUMAN	homo sapi
28	78.5	6.7	345	1	OPCM_RAT	rattus nor
29	78	6.6	485	1	SAHH_MESCR	mesembryan
30	78	6.6	3038	1	TRIO_HUMAN	homo sapi
31	77.5	6.6	226	1	C79H_HUMAN	homo sapi
32	77.5	6.6	345	1	OPCM_BOVIN	bos tauru
33	77.5	6.6	345	1	OPCM_HUMAN	homo sapi

34	77	6.6	109	1	KV01_RAT	P01681_rattus_norv
35	76.5	6.5	129	1	KV3M_HUMAN	P18136_homo_sapien
.36	76.5	6.5	120.3	1	PTC2_HUMAN	Q9Y4C5_homo_sapien
37	76	6.5	109	1	LV2E_HUMAN	P01708_homo_sapien
38	76	6.5	114	1	KV4A_HUMAN	P01625_homo_sapien
39	76	6.5	356.2	1	PGCV_CHICK	Q9053_gallus_gallus
40	75.5	6.4	108	1	KV1G_HUMAN	P01539_homo_sapien
41	75	6.4	149	1	KV5A_MOUSE	P01633_mus_musculus
42	75.5	6.4	485	1	SVAH_WHEAT	P32112_triticum_ae
43	75	6.4	112	1	KV2D_MOUSE	P01629_mus_musculus
44	75	6.4	115	1	KV3L_HUMAN	P04433_homo_sapien
45	75	6.4	117	1	KV1J_HUMAN	P01602_homo_sapien

110

RESULT 1
CTL4_HUMAN
ID CTL4_HUMAN
PRT; STANDARD;

P16410;
AC DT 01-AUG-1990 (Rel. 15, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED ANTIGEN 4) (CTTA-4) (C15orf52, CNTN4L, CD252, NTN4L)

US Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 1-37 FROM N.A.
MEDLINE=91318145; PubMed=1713603;
xx

Golstein P., Razzouk C., Rouvier E., Mattei M.-G., Luciani M.F.,
"CTLA-4 and CD28 activated lymphocyte molecules are closely related
in both mouse and human as to sequence, message expression, gene
structure, and chromosomal location." *J. Immunol.* 150: 1207-1211, 1993.

J. Immunol. 147:1037-1044 (1991).
 [2] J. Immunol. 147:1037-1044 (1991).
 SEQUENCE OF 38-223 FROM N.A.
 TISSUE-LYMPHOCYTES; PubMed=3220103;
 MEDLINE=89130925; Dariavach P., Mattei M.-G., Golstein P., Lefranc M.-P.;
 Human Ig superfamily CTLA-4 gene: chromosomal localization and
 identity of protein sequence in cytoplasmic domains; Eur. J. Immunol. 18:1905-1908,
 1988.

FUNCTION: RP XX
MEDLINE=91341416; PubMed=1714933;
Linsley P.S., Braddy W., Urnes M., Griosmaire L.S., Damle N.K.,
Ledbetter J.A.;
"CTLA-4 is a second receptor for the B cell activation antigen B7";
J EXP MED 1994 May; 189(5): 1551-5.

[4] N STRUCTURE BY NMR OF 37-165.
MEDLINE=97372889; PubMed=228944;
Metzler W.J., Bajorath J., Fenderson W., Shaw S.Y., Constantine K.L., Naemura J., Leytze G., Peach R.J., Lavoie T.B., Mueller L., Linsley P.S.; "Solution structure of human CTLA-4 and delineation of a CD80/CD86 binding site conserved in CD28"; Nat. Struct. Biol. 4:527-531(1997).
[5] C FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1 AND B7-2 (CD86).
[6] C SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
[7] C TISSUE SPECIFICITY: CELL SURFACE OF ACTIVATED T-LYMPHOCYTES.
[8] C SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
[9] C WWW=HTTP://WWW.PDB.ODD.UGA.EDU/CD152/entry/;
WWW=HTTP://WWW.PDB.ODD.UGA.EDU/CD152/entry/;

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(CD80) AND B7-2 (CD86) (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; M74363; AA52127.1; -.

DR EMBL; M37243; AA52773.1; JOINED.

DR EMBL; M37244; AA52773.1; JOINED.

DR PIR; S08614; S08614.

DR POR; 1AH1; 15-APR-94.

DR MIM; 123890; -.

DR InterPro; IPR003596; Ig_V.

DR SMART; SM00406; IgV; 1; T-cell; Transmembrane; Glycoprotein; Signal.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW POTENTIAL.

KW CYTOPLASMIC (POTENTIAL).

KW IG-LIKE V-TYPE DOMAIN.

KW BY SIMILARITY.

KW N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBONYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBONYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBONYD 223 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

KW DISULFID 85 103 BY SIMILARITY.

KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

KW DISULFID 85 103 BY SIMILARITY.

KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

KW DISULFID 85 103 BY SIMILARITY.

KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

KW DISULFID 85 103 BY SIMILARITY.

KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

KW DISULFID 85 103 BY SIMILARITY.

KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

KW DISULFID 85 103 BY SIMILARITY.

KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

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KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

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KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

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KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

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KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

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KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

KW DISULFID 85 103 BY SIMILARITY.

KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003007; Ig_1.

DR SMART; SM00405; Ig_1.

KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW SIGNAL 1 35 POTENTIAL.

KW CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

KW EXTRACELLULAR (POTENTIAL).

KW DOMAIN 189 189 CYTOPLASMIC (POTENTIAL).

KW DOMAIN 39 39 BY SIMILARITY.

KW DISULFID 85 103 BY SIMILARITY.

KW CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).

KW SEQUENCE 223 AA; 24430 MW; 2DDB865D871D8921 CRC64;

CC DR EMBL; AF281633; AAF86981.1; -.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; I

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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:00:52 ; Search time 54.19 Seconds
(without alignments)
601.933 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: MACLGFRKHKAQNLATRTW.....MPPTEPECEKQFQYFFIPIN 223

Scoring table: BLOSUM62

Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Actual number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_17:*

```

1: sp_archaea;*
2: sp_bacteria;*
3: sp_fungi;*
4: sp_human;*
5: sp_invertebrate;*
6: sp_mammal;*
7: sp_mhc;*
8: sp_organelle;*
9: sp_phage;*
10: sp_plant;*
11: sp_rhodent;*
12: sp_virus;*
13: sp_vertebrate;*
14: sp_unclassified;*

```

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1122	95.6	223	6 O9BDN7	O9bdn7 papio anubis
2	1118	95.2	223	6 Q9BDC4	Q9bdc4 macaca mulatta
3	1076	91.7	223	6 Q9BDP1	Q9bdp1 aotus trivirgatus
4	1034	88.1	223	6 Q9XTA1	Q9xta1 felis silvestris
5	1032	87.9	223	6 Q9TII02	Q9tii02 canis familiaris
6	1022	87.1	223	6 Q9GP2	Q9gp2 canis familiaris
7	1014	86.4	223	6 Q9XSY7	Q9xsy7 felis silvestris
8	1006	85.7	223	6 Q9N186	Q9n186 sus scrofa
9	997	84.9	223	6 Q9AS11	Q9as11 canis familiaris
10	996	84.8	223	1 Q9JLV3	Q9jlv3 marmota monax
11	984	83.8	221	6 Q9B9090	Q28090 bos taurus
12	975	83.0	221	6 Q97631	Q97631 ovis aries
13	896	76.3	223	11 Q92859	Q62859 rattus norvegicus
14	882	75.1	223	11 Q9QZZ7	Q9qzz7 mus musculus
15	592	50.4	137	4 Q9S653	Q9s653 homo sapiens
16	587	50.0	115	4 Q9BZK2	Q9bzk2 homo sapiens
17	534	45.5	174	11 Q9Z1A7	Q9z1a7 rattus norvegicus
18	442	37.6	84	4 Q9UKN9	Q9ukn9 homo sapiens
19	252	21.5	68	11 Q99PF8	Q99pf8 cricetus

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	223 AA.
ID	Q9BDN7			
QBDBNT				
AC				
DT	01-JUN-2001	(TREMBBLE! 17, Created)		
DT	01-JUN-2001	(TREMBBLE! 17, Last sequence update)		
DT	01-JUN-2001	(TREMBBLE! 17, Last annotation update)		
DE	CD1152	PROTEIN PRECURSOR.		
GN	CTLA-4			
OS	Papio anubis (Olive baboon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chordata; Catarrhini; Cercopithecoidea; Cercopithecine; Papio.			
OX	NCBI_TaxID=9555;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.; Cloning, sequencing and homology analysis of nonhuman primate Fas-Ligand and co-stimulatory molecules.			
RT	"Cloning, sequencing and homology analysis of nonhuman primate Fas-Ligand and co-stimulatory molecules."			
RL	Immunogenetics 0:0-0(2001); DR EMBL; AF344838; AAC37534.1; -.			
KW				
FT				
SQ	SEQUENCE 223 AA; EC18C279CCCC5668 CRC64;	37	POTENTIAL.	

QY	1 MACLGFORHKAQNLNATRTPCTLLFFLPVCKAMHVAOPAVVLAASSRGTSASFVEY 60	95.6%; Score 1122;	DB 6;	Length 223;
	Best Local Similarity 96.9%;	Pred. No. 4.6e-99;		
	Matches 216; Conservative 2;	Mismatches 5;	Indels 0;	Gaps 0;
	Signal 1	24655 MW;	EC18C279CCCC5668 CRC64;	
	SEQUENCE			

QY	181 LTAVSLSKMLKKRSPLTGVVVKMPPTECEKQFQPFYFIPIN	223	RN [1] SEQUENCE FROM N.A.
Db	181 LTAVSLSKMLKKRSPLTGVVVKMPPTECEKQFQPFYFIPIN	223	RP Willinger F.; Bostik P.; Mayne A.E.; King C.L.; Genain C.P.; RA Weiss W.R.; Ansari A.A.; "Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.";
RESULT	2		RT Immunogenetics 0:0-0/2001;
Q9BDC4	PRELIMINARY;	PRT; 223 AA.	RL EMBL; AF344834; AAK37530.1; -.
ID	Q9BDC4	POTENTIAL;	KW Signal.
AC	Q9BDC4;	PRT;	FT SIGNAL; 37 POTENTIAL.
DT	01-JUN-2001 (TREMBrel. 17, Created)	FT SIGNAL; 223 AA; 24813 MW;	FT SIGNAL; 223 AA; 24813 MW; 3F02052117C1431 CRC64;
DT	01-JUN-2001 (TREMBrel. 17, Last sequence update)	FT SIGNAL; 223 AA; 24813 MW;	FT SIGNAL; 223 AA; 24813 MW;
DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)	FT SIGNAL; 223 AA; 24813 MW;	FT SIGNAL; 223 AA; 24813 MW;
DE	CD152 PROTEIN PRECURSOR.		
GN	CTLA-4.		
OS	Macaca mulatta (Rhesus macaque), and Macaca nemestrina (Pig-tailed macaque), and Macaca fasciata (Red-crowned mangabey) (Sooty mangabey).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae; Macaca.		
OS	NCBI_TAXID=9544; 9545, 9531;		
RN	SEQUENCE FROM N.A.		
RC	SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;		
RA	Macaca nemestrina (Pig-tailed macaque), and Macaca fasciata (Red-crowned mangabey) (Sooty mangabey).		
RA	Willinger F.; Bostik P.; Mayne A.E.; King C.L.; Genain C.P.; Weiss W.R.; Ansari A.A.; "Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.";		
RA	Immunogenetics 0:0-0/2001;		
DR	EMBL; AF444646; AAK37530.1; -.		
DR	EMBL; AF344848; AAK37537.1; -.		
DR	EMBL; AF344848; AAK37608.1; -.		
KW	Signal.		
FT	VARIANT 223 AA; 223 MW;	POTENTIAL.	FT SIGNAL; 37 POTENTIAL.
FT	VARIANT 223 AA; 24683 MW;	N > D.	FT SIGNAL; 223 AA; 24683 MW; BDE42248A00396FA CRC64;
SQ	SEQUENCE 223 AA;		FT SIGNAL; 223 AA; 24683 MW; BDE42248A00396FA CRC64;
Query Match	95.28% Score 1118; DB 6; Length 223; Best Local Similarity 96.4%; Pred. No. 1.1e-98; Matches 215; Conservative 3; Misnatches 5; Indels 0; Gaps 0;		
QY	1 MACLGFORHKQAQLNLATRTWPCTTLLPFLFVFKPCKAMHYAQPAVVLASSRGIASFVCEY 60		
Db	1 MACLGFORHKQAQLNLATRTWPCTTLLPFLFVFKPCKAMHYAQPAVVLASSRGIASFVCEY 60		
QY	61 ASPGKATEVRVTYLQRADSQTVEVCAATYMGNGNQIYVTDPECPDSDTGTGGNQNLTIQGLR 120		
Db	61 ASPGKATEVRVTYLQRADSQTVEVCAATYMGNGNQIYVTDPECPDSDTGTGGNQNLTIQGLR 120		
QY	121 AMDGLYICKVEMYPPIYKRSPLITGVVYKMPPTPECEKFQPFYFIPIN 223		
Db	121 AMDGLYICKVEMYPPIYKRSPLITGVVYKMPPTPECEKFQPFYFIPIN 223		
RESULT	4		
Q9XTA1	PRELIMINARY;	PRT; 223 AA.	
ID	Q9XTA1;	PRELIMINARY;	
AC	Q9XTA1;	PRELIMINARY;	
DT	01-NOV-1999 (TREMBrel. 12, Created)		
DT	01-NOV-1999 (TREMBrel. 12, Last sequence update)		
DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)		
DE	CYTOTOXIC T-LYMPHOCYTE ASSOCIATED 4 (COSTIMULATORY MOLECULE B7 RECEPTOR CD152).		
GN	CTLA4 OR CTLA-4 OR CD152.		
OS	Felis silvestris catus (Cat).		
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
OC	Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E., Mikami T., Takahashi E.; "Molecular cloning and sequencing of a cDNA encoding the feline cytotoxic T-lymphocyte-associated 4 (CTLA4) homologue;" Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.		
RN	SEQUENCE FROM N.A.		
RA	Miyazawa Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E., Nishimura Y., "Molecular cloning and sequencing of a cDNA encoding the feline cytotoxic T-lymphocyte-associated 4 (CTLA4) homologue;" Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.		
RN	SEQUENCE FROM N.A.		
RA	Cho I.-S., Hash S., Collisson E.W.; "Sequence analyses of the feline Cd28 and CTRA-1;" Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.		
RN	SEQUENCE FROM N.A.		
RA	SEQUENCE FROM N.A.		
RA	Yang S., Sim G.-K.; "Nucleotide and Predicted Amino Acid Sequences of Canine and Feline CD152 (CTLA4)."		
RT	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.		
RT	- - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.		
CC			
DR	EMBL; AB02395; BAA82273.1; -.		
DR	EMBL; AF170725; ADD50988.1; -.		
DR	EMBL; AF15844; ARG43372.1; -.		
DR	HSSP; P16410; IAHL.		
DR	InterPro; IPR003599; Ig.		
NCBI_TAXID=9505;			

Scoring table:											
Title:		US-09-772-103-2		Gapext 0 .5							
Perfect score:		1174		522463 seqs, 74073290 residues							
Sequence:		1 MACLGFORHKAQQLNIAATRW MPPTEPECEKOFQPYFIPIN 223 306.406 Million cell updates/sec									
Post-processing: Minimum Match 0%											
Maximum Match 100%											
Listing first 45 summaries											
Database : A_Geneseq_1101:*											
1:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1980.DAT:*					RESULT 1					
2:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1981.DAT:*					AAG66519					
3:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1982.DAT:*					ID AAG66519 standard; Protein; 223 AA.					
4:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1983.DAT:*					XX					
5:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1984.DAT:*					AC AAG66519;					
6:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1985.DAT:*					XX					
7:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1986.DAT:*					DT 22-OCT-2001 (first entry)					
8:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1987.DAT:*					XX					
9:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1988.DAT:*					DE Human CTLA4.					
10:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1989.DAT:*					XX					
11:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1990.DAT:*					XX					
12:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1991.DAT:*					XX					
13:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1992.DAT:*					XX					
14:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1993.DAT:*					XX					
15:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1994.DAT:*					XX					
16:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1995.DAT:*					XX					
17:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1996.DAT:*					XX					
18:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1997.DAT:*					XX					
19:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1998.DAT:*					XX					
20:	/SIDSB8/gcgdata/geneseq/geneseqp/AA1999.DAT:*					XX					
21:	/SIDSB8/gcgdata/geneseq/geneseqp/AA2000.DAT:*					XX					
22:	/SIDSB8/gcgdata/geneseq/geneseqp/AA2001.DAT:*					XX					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
Result No.	Score	Query	Match Length	DB ID	Description						
1	1174	100.0	223	22 AAG66519	Human CTLA4, Homo	XX					
2	1170	99.7	223	21 AAY15129	Human CTLA4, soluble human CTLA4 protein	XX					
3	1159	98.7	223	18 AAW25111	Human CTLA4 protein	XX					
4	1159	98.7	223	22 AAU00687	Human CTLA4 protein	XX					
5	1103.5	94.0	234	20 AAY41133	Feline CTLA4 protein	PI					
6	1034	88.1	223	20 AAY41084	Canine CTLA4 protein	PI					
7	1022	87.1	223	20 AAY41083	Feline CTLA4 protein	XX					
8	1015	86.5	223	21 AAY32287	Cat CTLA-4 receptor	DR					
9	1015	86.5	223	21 AAY32280	Porcine CTLA-4 sol	DR					
10	1006	85.7	223	21 AAY15122	Human CTLA4 receptor	XX					
11	984.5	83.9	211	20 AAW8750	Novel antibody-toxic group conjugate comprising an antibody that	PT					

PR recognizes a molecule expressed only on activated T cells, useful for modulating immune response for treating autoimmune disorder, allergic response.

XX Example 3; Page 114-115; 123pp; English.

CC The invention relates to an antibody-toxic group conjugate comprising an antibody that specifically recognises a molecule expressed only on activated T cells, and a toxic group. The T cell molecule is preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4). CC The antibody of the invention is a humanised anti-CTLA4 antibody comprising a sequence of 128 or 142 amino acids fully defined in the CC specification. The antibody-toxic group conjugate is useful for modulating the immune response in a subject suffering from a disorder CC or condition such as autoimmune disorder, immune response to a graft, CC allergic response or an immune response to a therapeutic protein. CC The antibody is also useful for research purposes, e.g., in staining CC and isolating CTLA4-bearing cells, the antibody is also useful for CC T-cell typing, for isolating specific IL-2 receptor-bearing cells or CC fragments of the receptor, for vaccine preparation, and for determining CC the effectiveness of an agent to down regulate CTLA4 activity. The present sequence is human CTLA4, which is bound by the antibody CC provided in the invention.

XX Sequence 223 AA;

SQ Sequence 223 AA;

Query Match	100.0%	Score 1174;	DB 22;	Length 223;	
Best Local Similarity	100.0%	Pred. No. 3e-106;			
Matches	223;	Conservative 0;	Mismatches 0;	Gaps 0;	
QY	1	MACIGFQRHKAQINLATRWPCTLFFLPIPFCKAMHVQPAVVLASSRGIASFVEY	60		
Db	1	macigfqrhkqinlatrwpctlfflpipfckamhvqpaavvlassrgiasfvey	60		
QY	61	ASPGKATEVRVTYLROADSQVTECAATYMMGNELTFLDDSDTCGTSSGNOVNLTIQGLR	120		
Db	61	aspkgatervtvtvlroadsqvtecaatymmgnefltdsdcgtssgnvnltiqglr	120		
QY	61	AMDGLYICKVELMPPPYLGICNGAQIYVIDBEPCPDSDFLIWILAVSSGLIFFYSRL	180		
Db	61	amdglyickvelmppylgicngaqiyvidbepcpdsdfliwilaavssgiffysrl	180		
QY	121	AMDGLYICKVELMPPPYLGICNGAQIYVIDBEPCPDSDFLIWILAVSSGLIFFYSRL	180		
Db	121	amdglyickvelmppylgicngaqiyvidbepcpdsdfliwilaavssgiffysrl	180		
QY	181	LTAVALSKMLKRSPLTTGIVVKRPPTEPECEKFQPYFPIN	223		
Db	181	ltavlskmkrsplttgivvkppptepecekfqpyfpin	223		
		RESULT 3			
		AAW25111	AA.		
ID	5129	AAW25111 standard; protein; 223 AA.			
XX					
ID	AY15129	AY15129 standard; protein; 223 AA.			
XX					
ID	AY15129;				
XX					
DT	07-FEB-2000	(first entry)			
XX					
DE	Human CTLA-4 protein.				
XX					
KW	Human CTLA-4; soluble protein; xenograft; organ transplant; B7; CD28; KW xenograft-specific immunosuppression; recipient T-cell; energy; KW co-stimulatory signal 2; homology; porcine CTLA-4.				
XX					
OS	Homo sapiens.				
XX					
PH	Key Peptide	Location/Qualifiers 1..37			
FT		/label= Signal_peptide			
FT		38..234			
FT		Protein			
FT		/label= mat_protein			
FT		62..67			
FT		Region			
FT		/note= "CDR 1-like region"			
FT		86..90			
FT		/note= "CDR 2-like region"			
FT		132..139			
FT		Region			
FT		/note= "CDR 3-like region; highly conserved"			